



## SEQUENCE LISTING

<110> Apicella, M.A.  
Sunshine, M.G.  
Lee, N.  
Gibson, B.  
Arumugham, R.

<120> Non-toxic mutants of pathogenic gram-negative bacteria

<130> 875.001US2

<140> US 09/077,572

<141> 1998-10-13

<150> PCT/US96/18984

<151> 1996-11-27

<150> US 08/565,943

<151> 1995-12-01

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<212> DNA

<213> Haemophilus influenzae, strain 2019

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caa ttt caa ccg cac ttt tta gcc cca aaa tac tgg ctt ttt tgg cta 102  
Gln Phe Gln Pro His Phe Leu Ala Pro Lys Tyr Trp Leu Phe Trp Leu  
10 15 20

ggc gtg gca att tgg cga agt att tta tgt ctt ccc tat cct att ttg 150  
Gly Val Ala Ile Trp Arg Ser Ile Leu Cys Leu Pro Tyr Pro Ile Leu  
25 30 35

cgc cat att ggt cat ggt ttc ggt tgg ctg ttt tca cat tta aaa gtg 198  
Arg His Ile Gly His Gly Phe Gly Trp Leu Phe Ser His Leu Lys Val  
40 45 50 55

ggc aaa cgt cga gct gcc att gca cgc cgt aat ctt gaa ctt tgt ttc 246  
Gly Lys Arg Arg Ala Ala Ile Ala Arg Arg Asn Leu Glu Leu Cys Phe  
60 65 70

cct gat atg cct gaa aac gaa cgt gag acg att ttg caa gaa aat ctt 294  
Pro Asp Met Pro Glu Asn Glu Arg Glu Thr Ile Leu Gln Glu Asn Leu  
75 80 85

cgt tca gta ggc atg gca att atc gaa act ggc atg gct tgg ttt tgg 342  
Arg Ser Val Gly Met Ala Ile Ile Glu Thr Gly Met Ala Trp Phe Trp  
90 95 100

tcg gat tca cgt atc aaa aaa tgg tcg aaa gtt gaa ggc tta cat tat	390
Ser Asp Ser Arg Ile Lys Lys Trp Ser Lys Val Glu Gly Leu His Tyr	
105 110 115	
cta aaa gaa aat caa aaa gat gga att gtt ctc gtc ggc gtt cat ttc	438
Leu Lys Glu Asn Gln Lys Asp Gly Ile Val Leu Val Gly Val His Phe	
120 125 130 135	
tta acg cta gaa ctt ggc gca cgc atc att ggt tta cat cat cct ggc	486
Leu Thr Leu Glu Leu Gly Ala Arg Ile Ile Gly Leu His His Pro Gly	
140 145 150	
att ggt gtt tat cgt cca aat gat aat cct ttg ctt gat tgg cta caa	534
Ile Gly Val Tyr Arg Pro Asn Asp Asn Pro Leu Leu Asp Trp Leu Gln	
155 160 165	
aca caa ggc cgt tta cgc tcc aat aaa gat atg ctt gat cgt aaa gat	582
Thr Gln Gly Arg Leu Arg Ser Asn Lys Asp Met Leu Asp Arg Lys Asp	
170 175 180	
tta cgc gga atg atc aaa gct tta cgc cac gaa gaa acc att tgg tat	630
Leu Arg Gly Met Ile Lys Ala Leu Arg His Glu Glu Thr Ile Trp Tyr	
185 190 195	
gcg cct gat cac gat tac ggc aga aaa aat gcc gtt ttt gtt cct ttt	678
Ala Pro Asp His Asp Tyr Gly Arg Lys Asn Ala Val Phe Val Pro Phe	
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ttt gca gta cct gac act tgc act act act ggt agt tat tat tta ttg	726
Phe Ala Val Pro Asp Thr Cys Thr Thr Thr Gly Ser Tyr Tyr Leu Leu	
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Lys Ser Ser Gln Asn Ser Lys Val Ile Pro Phe Ala Pro Leu Arg Asn	
235 240 245	
aaa gat ggt tca ggc tat acc gtg agc att tca gcg cct gtt gat ttt	822
Lys Asp Gly Ser Gly Tyr Thr Val Ser Ile Ser Ala Pro Val Asp Phe	
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Thr Asp Leu Gln Asp Glu Val Ala Ile Ala Val Arg Met Asn Gln Ile	
265 270 275	
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Val Glu Lys Glu Ile Met Lys Gly Ile Ser Gln Tyr Met Trp Leu His	
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30

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